

#8



032301.195.seq.ST25.txt  
SEQUENCE LISTING

<110> MOCKEL Bettina et al.

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE cstA GENE

<130> 032301 WD 195

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 2718

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (200)..(2515)

<223>

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20

tggccgaact ttcctttttc tgcattgcatt tctgcacaca gtttctgccc gctgtttctg 1  
80

cccgtgttt ctacgcata gtg gct ttg aaa cga ccc gaa gag aaa aca gta 2  
32

Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val

1 5 10

aag atc gtg acc ata aaa cag act gac aac atc aat gac gat gat ttg 2  
80

Lys Ile Val Thr Ile Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu

15 20 25

gtg tac agc aac gct act gac ctt cca gta ggc gtg aag aag tcc cct 3

## 032301.195.seq.ST25.txt

28

Val Tyr Ser Asn Ala Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro

30

35

40

aaa atg tca ccg acc gcc cgc gtt ggt ctc ctt gtc ttt ggg gtt atc 3

76

Lys Met Ser Pro Thr Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile

45

50

55

gcg gcg gtg ggt tgg gga gca atc gct ttc tcc cgt ggc gaa aca atc 4

24

Ala Ala Val Gly Trp Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile

60

65

70

75

aac tct gtg tgg ctg gtt ttg gcg gca gtt ggt tcc tat atc att gcg 4

72

Asn Ser Val Trp Leu Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala

80

85

90

ttt tct ttc tat gcc cga ctg att gaa tac aaa gtt gtt aag ccg aaa 5

20

Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys

95

100

105

gat cag cga gca acc ccg gcg gaa tac gtt aat gac ggc aag gac tat 5

68

Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr

110

115

120

gtc cca acg gat cgt cgt gtg ctt ttt ggc cac cac ttt gca gct att 6

16

Val Pro Thr Asp Arg Arg Val Leu Phe Gly His His Phe Ala Ala Ile

125

130

135

032301.195.seq.ST25.txt

gca ggt gcc ggt cca ttg gtt gga cct gtc atg gcc gcg cag atg ggc 64	6
Ala Gly Ala Gly Pro Leu Val Gly Pro Val Met Ala Ala Gln Met Gly	
140                      145                      150                      155	
tac ctg cca ggc acc ttg tgg att atc ctc ggt gtg att ttc gcc ggt 12	7
Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly	
160                      165                      170	
gca gtg cag gac tac cta gtg ctg tgg gtg tct act cgt agg cgt gga 60	7
Ala Val Gln Asp Tyr Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly	
175                      180                      185	
cgc tca ctt ggc cag atg gtt cgt gat gaa atg ggc acg gtc ggt gga 08	8
Arg Ser Leu Gly Gln Met Val Arg Asp Glu Met Gly Thr Val Gly Gly	
190                      195                      200	
gct gcc ggt atc ttg gcg acc atc tcc atc atg atc atc att atc gcg 56	8
Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala	
205                      210                      215	
gtg ctc gca ttg atc gtg gtt aat gca ctg gct gat tca cca tgg ggc 04	9
Val Leu Ala Leu Ile Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly	
220                      225                      230                      235	
gtt ttc tcc atc acc atg acc atc cca att gca ctg ttc atg ggt gtg 52	9
Val Phe Ser Ile Thr Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val	
240                      245                      250	

032301.195.seq.ST25.txt

tac ttg cgt tac ctg cgc cca ggt cgt gtt act gaa gtg tcc atc atc 10  
00

Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile

255

260

265

ggt gtg gca ctg ctc ctg ctg gct atc gtt gct ggt ggt tgg gtt gca 10  
48

Gly Val Ala Leu Leu Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala

270

275

280

gac acc tca tgg ggc gtg gaa tgg ttc acc tgg tct aag acc act ttg 10  
96

Asp Thr Ser Trp Gly Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu

285

290

295

gcg ttg gcc ttg atc ggt tac gga atc atg gct gcg att ttg ccg gtg 11  
44

Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val

300

305

310

315

tgg ctg ctg ctt gca ccg cgc gat tac ctg tct acc ttt atg aag atc 11  
92

Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile

320

325

330

ggc gtc atc ggt ctg ttg gca gtg ggt att ttg ttc gca cgt cct gag 12  
40

Gly Val Ile Gly Leu Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu

335

340

345

gtg cag atg cct tcc gtg acc tcc ttc gca ctt gag ggc aac ggt ccg 12  
88

Val Gln Met Pro Ser Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro

350

355

360

032301.195.seq.ST25.txt

gtg ttc tct gga agt ctg ttc cca ttc ctg ttc atc acg att gcc tgt	13
36	
Val Phe Ser Gly Ser Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys	
365	370
375	
ggt gca ctg tct ggt ttc cac gca ctg att tct tca gga acc aca cca	13
84	
Gly Ala Leu Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro	
380	385
390	395
aag ctt gtg gag aag gaa tcc cag atg cgc atg ctc ggc tac ggc ggc	14
32	
Lys Leu Val Glu Lys Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly	
400	405
410	
atg ttg atg gaa tct ttc gtg gcg atg atg gca ctg atc acc gct gtt	14
80	
Met Leu Met Glu Ser Phe Val Ala Met Met Ala Leu Ile Thr Ala Val	
415	420
425	
att ctg gat cgt cac ctg tac ttc tcc atg aac gct ccg ctg gca ctg	15
28	
Ile Leu Asp Arg His Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu	
430	435
440	
act ggt gga gat cca gca acc gca gct gag tgg gtt aac tcc att ggg	15
76	
Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly	
445	450
455	
ctg aca ggt gcg gat atc acc ccg gaa cag ctg tcg gaa gct gct gaa	16
24	
Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu	

460

465

470

475

agt gtc gga gaa tcc act gtt att tcc cgt acc ggt ggc gca cca acc 16  
72

Ser Val Gly Glu Ser Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr

480

485

490

ttg gcg ttc ggt atg tct gaa atc ctc tcc gga ttc atc ggc ggc gct 17  
20

Leu Ala Phe Gly Met Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala

495

500

505

gga atg aag gcg ttc tgg tac cac ttc gcc atc atg ttt gag gct ctg 17  
68

Gly Met Lys Ala Phe Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu

510

515

520

ttc atc ctc act act gtg gat gca ggt act cgt gtg gct cgc ttt atg 18  
16

Phe Ile Leu Thr Thr Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met

525

530

535

atg acc gat acc ttg ggc aat gtt cca ggt ctg cgc cgt ttc aag gat 18  
64

Met Thr Asp Thr Leu Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp

540

545

550

555

cct tca tgg act gtc ggt aac tgg att tct acc gtg ttt gtg tgt gct 19  
12

Pro Ser Trp Thr Val Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala

560

565

570

cta tgg ggt gct att ttg ctc atg ggt gtt acc gat cca ctg ggc ggc 19  
60

Leu Trp Gly Ala Ile Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly

## 032301.195.seq.ST25.txt

575

580

585

atc aac gtg ctt ttc cca cta ttc ggt atc gct aac cag ctg ctc gcc 20  
08

Ile Asn Val Leu Phe Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala

590

595

600

gct att gca ctt gct ctc gtg ctg gtt gtt gtg gtg aag aag ggc ctg 20  
56

Ala Ile Ala Leu Ala Leu Val Leu Val Val Val Val Lys Lys Gly Leu

605

610

615

tac aag tgg gcg tgg att cca gct gtt cct ttg gca tgg gat ctc att 21  
04

Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile

620

625

630

635

gtc acg atg act gcg tca tgg cag aag att ttc cac tct gat ccg gct 21  
52

Val Thr Met Thr Ala Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala

640

645

650

att ggc tac tgg gct cag aac gcg aac ttc cgc gat gca aag tct caa 22  
00

Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln

655

660

665

ggc ctt acc gaa ttt ggt gcc gct aaa tct cct gag gca atc gat gcg 22  
48

Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala

670

675

680

gtt atc cga aac acc atg att cag ggc atc ttg tcc atc ctg ttc gcg 22  
96

## 032301.195.seq.ST25.txt

Val Ile Arg Asn Thr Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala

685

690

695

gtg ctc gtc ctc gtt gtt gtc ggc gca gcc att gcg gtg tgc atc aag 23  
44

Val Leu Val Leu Val Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys

700

705

710

715

tcc atc agg gct cgt gca gcc gga aca cct ttg gag acc act gaa gag 23  
92

Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu

720

725

730

cct gat act gaa tct gag ttc ttc gcc cca act gga ttc ctt gca tct 24  
40

Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser

735

740

745

tcc agg gat aag gaa gtc cag gcc atg tgg gac gag cgc tac cca ggc 24  
88

Ser Arg Asp Lys Glu Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly

750

755

760

ggt gcg ccc gtg tct tct gga ggg cac taaaacatga tggctcttac 25  
35

Gly Ala Pro Val Ser Ser Gly Gly His

765

770

tcatgcactg tggaaaatcc cgcgggcggt gtggtggtat ctactgagc tcatggggga 25  
95

cacggcgtat toccaagtatg tgggtgcactt aaagcaccac catccggatg ctccgattcc 26  
55

tactgagcgg gagtattggc gggcaaagta tgcagatcag gacgctaadc ctggtgccccg 27  
15



ctg  
18

<210> 2  
<211> 772  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 2

Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile  
1 5 10 15

Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala  
20 25 30

Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr  
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp  
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu  
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala  
85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr  
100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg  
115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro  
130 135 140

032301.195.seq.ST25.txt

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr  
145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr  
165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln  
180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu  
195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile  
210 215 220

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr  
225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu  
245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu  
260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly  
275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile  
290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala  
305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu  
325 330 335

## 032301.195.seq.ST25.txt

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser  
 340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser  
 355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly  
 370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys  
 385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser  
 405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His  
 420 425 430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro  
 435 440 445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp  
 450 455 460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser  
 465 470 475 480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met  
 485 490 495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe  
 500 505 510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr  
 515 520 525

## 032301.195.seq.ST25.txt

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu  
 530 535 540

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val  
 545 550 555 560

Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile  
 565 570 575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe  
 580 585 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala  
 595 600 605

Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp  
 610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala  
 625 630 635 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala  
 645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe  
 660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr  
 675 680 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val  
 690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg  
 705 710 715 720

032301.195.seq.ST25.txt

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser  
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu  
740 745 750

Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser  
755 760 765

Ser Gly Gly His  
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<213> Corynebacterium glutamicum

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20

ggtatgacta gcccactct aaatgggtgt 1  
49

<210> 4  
<211> 2867  
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<213> Corynebacterium glutamicum

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<222> (349)..(2664)  
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20

ggatgacta gccccactct aaatggtgta ggatggtata aatcatctct caatgttact 1  
80

tttccattgt taagaattaa caactctcgg tgatttgctg catacccagc tgtcaaagat 2  
40

ccgatcatcg gcatacagaa acacccatct ggccgaactt tcctttttct gcatgcattt 3  
00

ctgcacacag tttctgcccc ctgtttctgc ccgctgtttc tacgcata gtg gct ttg 3  
57

Met Ala Leu

1

aaa cga ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act 4  
05

Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr

5

10

15

gac aac atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt 4  
53

Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu

20

25

30

35

cca gta ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt 5  
01

Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val

40

45

50

ggc ctc ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc 5  
49

Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile

55

60

65

gct ttc tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg 5  
97

032301.195.seq.ST25.txt

Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala  
 70 75 80

gca gtt ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att 6  
 45  
 Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile  
 85 90 95

gaa tac aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa 6  
 93  
 Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu  
 100 105 110 115

tac gtt aat gac ggc aag gac tat gtc cca acg gat cgt cgt gtg ctt 7  
 41  
 Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu  
 120 125 130

ttt ggc cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga 7  
 89  
 Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly  
 135 140 145

cct gtc atg gcc gcg cag atg ggc tac ctg cca ggc acc ttg tgg att 8  
 37  
 Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile  
 150 155 160

atc ctc ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg 8  
 85  
 Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu  
 165 170 175

tgg gtg tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt 9

## 032301.195.seq.ST25.txt

33

Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg

180

185

190

195

gat gaa atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc

81

9

Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile

200

205

210

tcc atc atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat

29

10

Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn

215

220

225

gca ctg gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc

77

10

Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile

230

235

240

cca att gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt

25

11

Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly

245

250

255

cgt gtt act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct

73

11

Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala

260

265

270

275

atc gtt gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg

21

12

Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp

280

285

290



## 032301.195.seq.ST25.txt

ttc acc tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga 12  
69

Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly

295

300

305

atc atg gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat 13  
17

Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp

310

315

320

tac ctg tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg 13  
65

Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu Leu Ala Val

325

330

335

ggt att ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc 14  
13

Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser Val Thr Ser

340

345

350

355

ttc gca ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca 14  
61

Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro

360

365

370

ttc ctg ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca 15  
09

Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala

375

380

385

ctg att tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag 15  
57

Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln

390

395

400

032301.195.seq.ST25.txt

atg cgc atg ctc ggc tac ggc ggc atg ttg atg gaa tct ttc gtg gcg 16  
05

Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser Phe Val Ala

405

410

415

atg atg gca ctg atc acc gct gtt att ctg gat cgt cac ctg tac ttc 16  
53

Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His Leu Tyr Phe

420

425

430

435

tcc atg aac gct ccg ctg gca ctg act ggt gga gat cca gca acc gca 17  
01

Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro Ala Thr Ala

440

445

450

gct gag tgg gtt aac tcc att ggg ctg aca ggt gcg gat atc acc ccg 17  
49

Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp Ile Thr Pro

455

460

465

gaa cag ctg tcg gaa gct gct gaa agt gtc gga gaa tcc act gtt att 17  
97

Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser Thr Val Ile

470

475

480

tcc cgt acc ggt ggc gca cca acc ttg gcg ttc ggt atg tct gaa atc 18  
45

Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met Ser Glu Ile

485

490

495

ctc tcc gga ttc atc ggc ggc gct gga atg aag gcg ttc tgg tac cac 18  
93

Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe Trp Tyr His

500

505

510

515

ttc gcc atc atg ttt gag gct ctg ttc atc ctc act act gtg gat gca 41	19
Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr Val Asp Ala	
520 525 530	
ggt act cgt gtg gct cgc ttt atg atg acc gat acc ttg ggc aat gtt 89	19
Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val	
535 540 545	
cca ggt ctg cgc cgt ttc aag gat cct tca tgg act gtc ggt aac tgg 37	20
Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val Gly Asn Trp	
550 555 560	
att tct acc gtg ttt gtg tgt gct cta tgg ggt gct att ttg ctc atg 85	20
Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile Leu Leu Met	
565 570 575	
ggt gtt acc gat cca ctg ggc ggc atc aac gtg ctt ttc cca cta ttc 33	21
Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe	
580 585 590 595	
ggt atc gct aac cag ctg ctc gcc gct att gca ctt gct ctc gtg ctg 81	21
Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu	
600 605 610	
gtt gtt gtg gtg aag aag ggc ctg tac aag tgg gcg tgg att cca gct 29	22
Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala	

615

620

625

gtt cct ttg gca tgg gat ctc att gtc acg atg act gcg tca tgg cag 22  
77

Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala Ser Trp Gln

630

635

640

aag att ttc cac tct gat ccg gct att ggc tac tgg gct cag aac gcg 23  
25

Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala Gln Asn Ala

645

650

655

aac ttc cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct 23  
73

Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala

660

665

670

675

aaa tct cct gag gca atc gat gcg gtt atc cga aac acc atg att cag 24  
21

Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln

680

685

690

ggc atc ttg tcc atc ctg ttc gcg gtg ctc gtc ctc gtt gtt gtc ggc 24  
69

Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Val Gly

695

700

705

gca gcc att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga 25  
17

Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly

710

715

720

aca cct ttg gag acc act gaa gag cct gat act gaa tct gag ttc ttc 25  
65

Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe

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725

730

735

gcc cca act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc 26  
13

Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala

740

745

750

755

atg tgg gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg 26  
61

Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly

760

765

770

cac taaaacatga tggctcttac tcatgcactg tggaaaatcc cgcgggcggt 27  
14

His

gtggtggtat ctactgagc tcatggggga cacggcgtat tccaagtatg tgggtgcactt 27  
74

aaagcaccac catccggatg ctccgattcc tactgagcgg gagtattggc gggcaaagta 28  
34

tgcagatcag gacgctaata ctggtgcccg ctg 28  
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<212> PRT

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<400> 5

Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile  
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Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala  
20 25 30

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Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr  
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp  
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu  
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala  
85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr  
100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg  
115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro  
130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr  
145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr  
165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln  
180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu  
195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile  
210 215 220

032301.195.seq.ST25.txt

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr  
225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu  
245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu  
260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly  
275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile  
290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala  
305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu  
325 330 335

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser  
340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser  
355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly  
370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys  
385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser  
405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His  
                   420                                  425                                  430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro  
                   435                                  440                                  445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp  
                   450                                  455                                  460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser  
                   465                                  470                                  475                                  480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met  
                                   485                                  490                                  495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe  
                                   500                                  505                                  510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr  
                   515                                  520                                  525

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu  
                   530                                  535                                  540

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val  
                   545                                  550                                  555                                  560

Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile  
                                   565                                  570                                  575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe  
                                   580                                  585                                  590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala  
                   595                                  600                                  605



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Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp  
610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala  
625 630 635 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala  
645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe  
660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr  
675 680 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val  
690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg  
705 710 715 720

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser  
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu  
740 745 750

Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser  
755 760 765

Ser Gly Gly His  
770

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<211> 20

032301.195.seq.ST25.txt

<212> DNA

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<400> 6

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<210> 7

<211> 20

<212> DNA

<213> *Corynebacterium glutamicum*

<400> 7

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20